FIG. 1

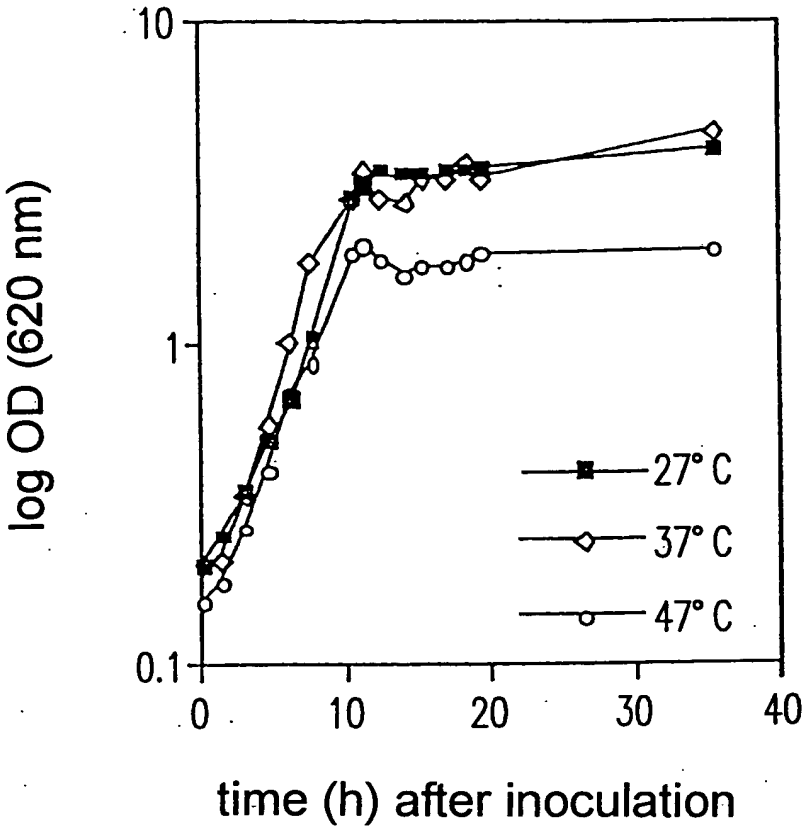
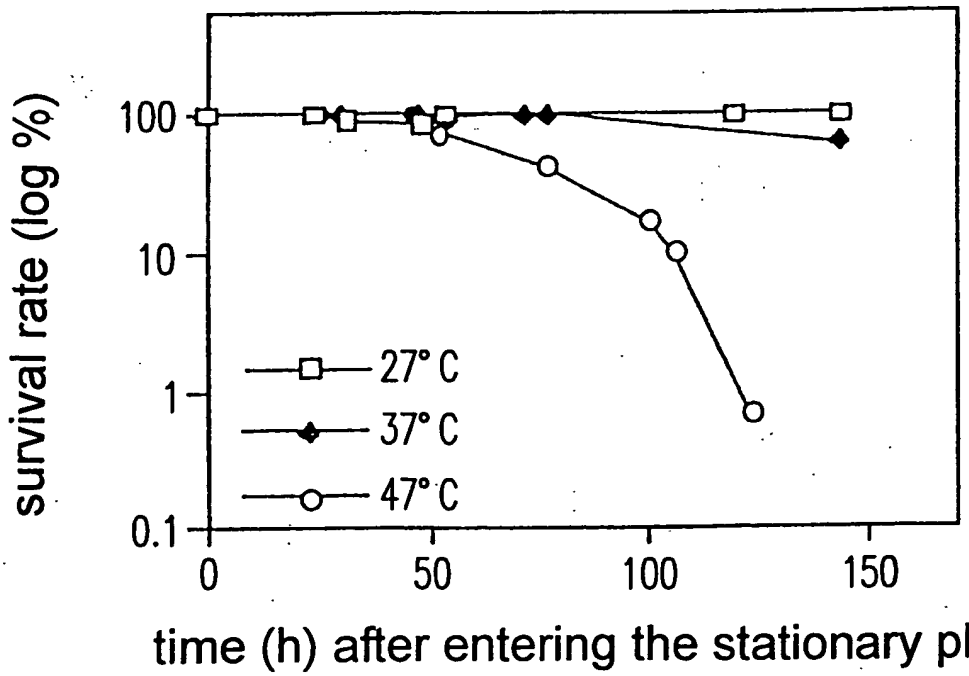

10
1
0.1
log OD (620 nm)
0
10
20
30
40
time (h) after inoculation
27° C
37° C
47° C

FIG. 2


100
10
1
0.1
survival rate (log %)
0
50
100
150
time (h) after entering the stationary phase
27° C
37° C
47° C

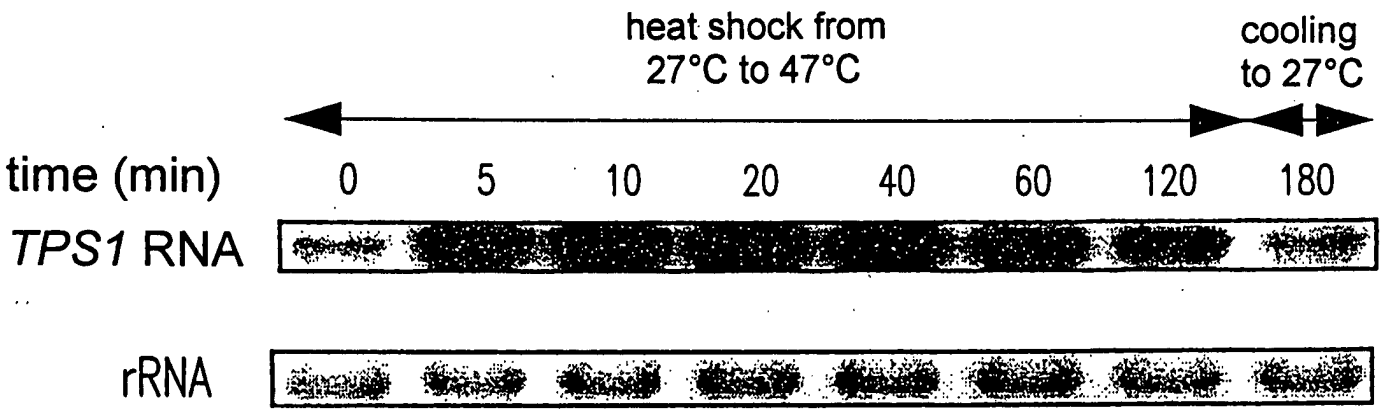


FIG. 3A

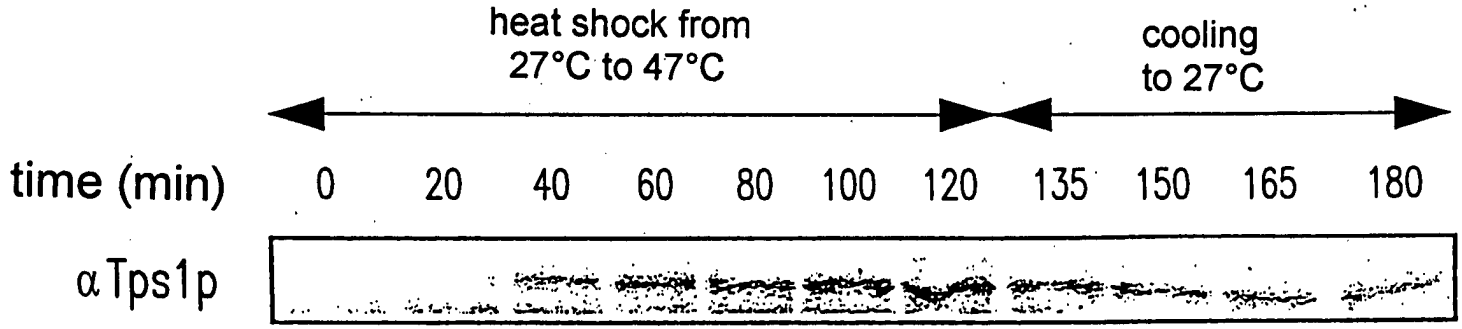


FIG. 3B

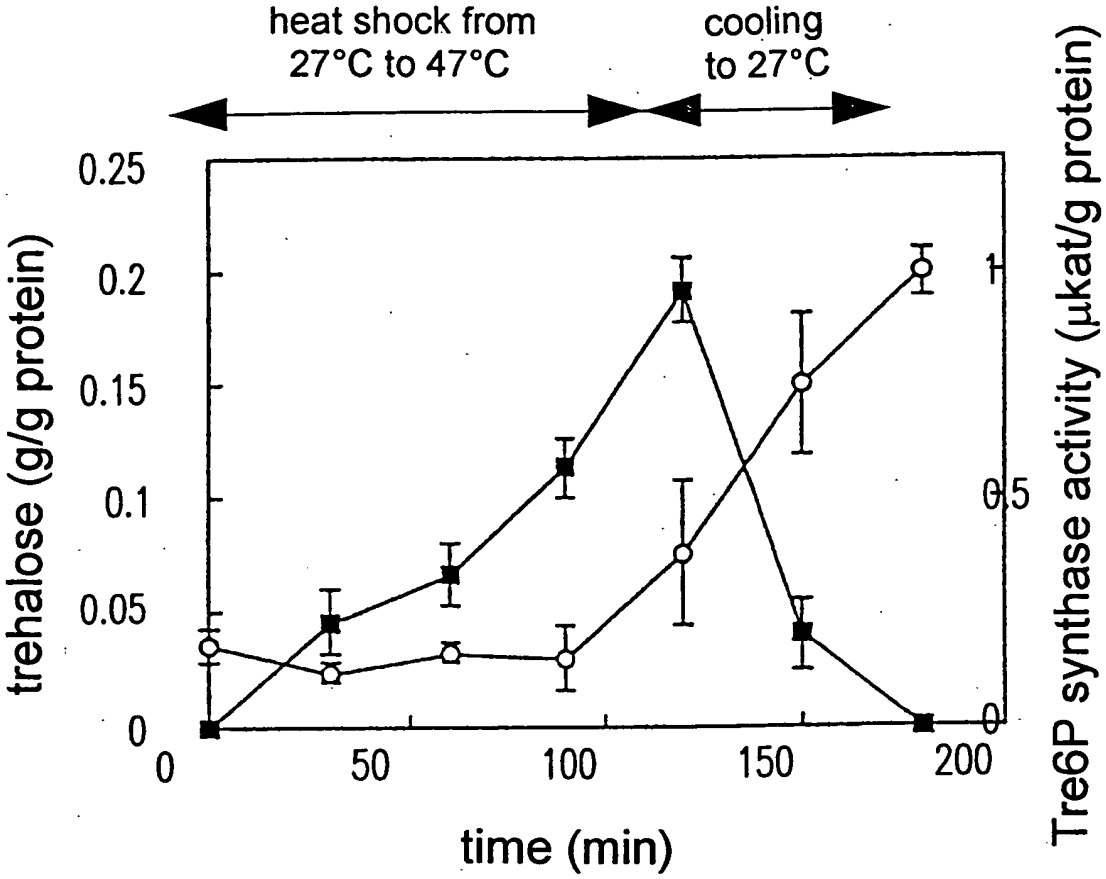

heat shock from
27°C to 47°C
cooling
to 27°C
trehalose (g/g protein)
0.25
0.2
0.15
0.1
0.05
0
0
50
100
150
200
time (min)
1
0.5
0
Tre6P synthase activity (µkat/g protein)

FIG. 3C

FIG. 4A

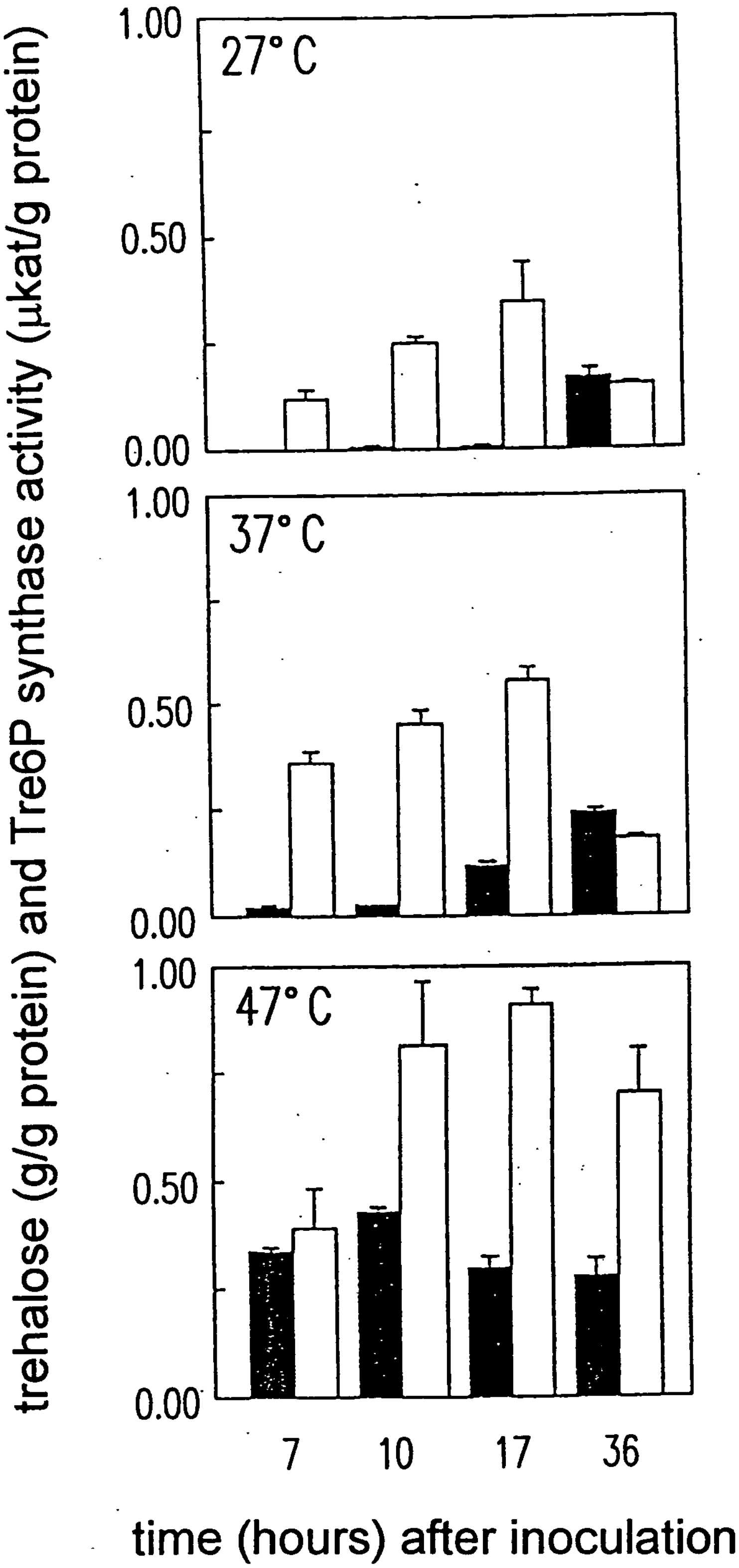


FIG. 4B

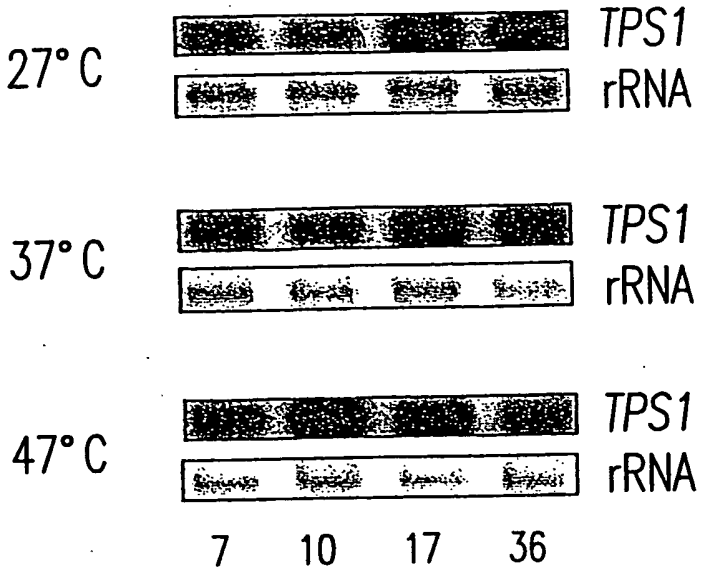
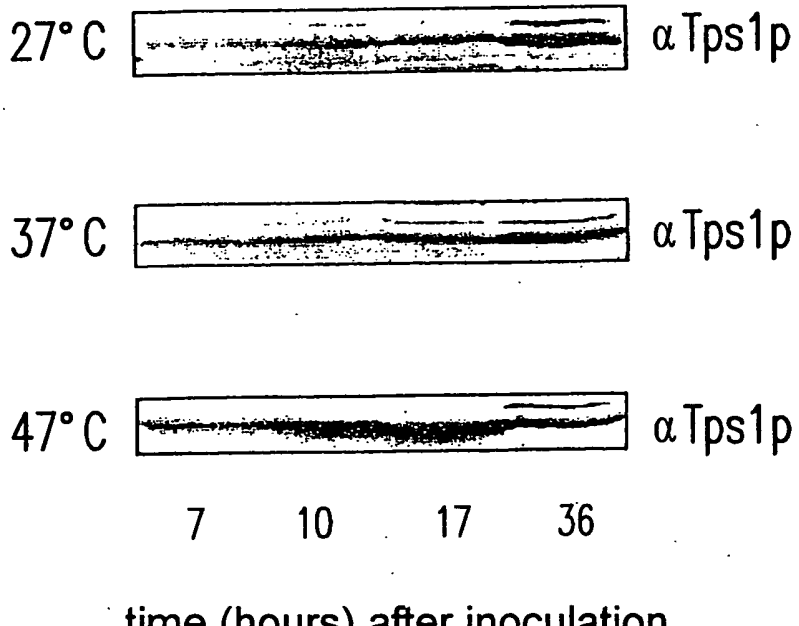
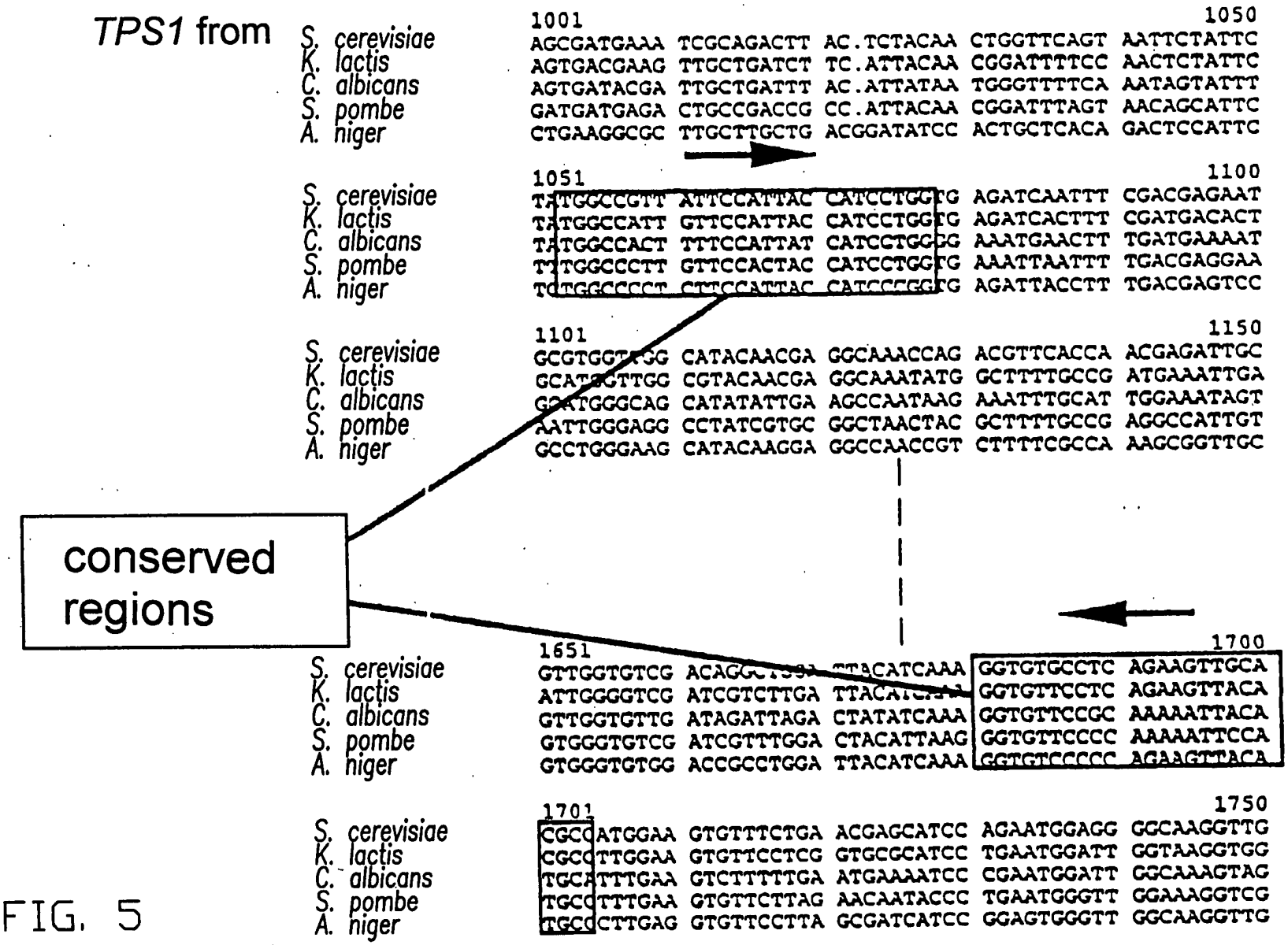

27° C
TPS1
rRNA
37° C
TPS1
rRNA
47° C
TPS1
rRNA
7
10
17
36
time (hours) after inoculation

FIG. 4C


27° C
αTps1p
37° C
αTps1p
47° C
αTps1p
7
10
17
36
time (hours) after inoculation


TPS1 from
S. cerevisiae
K. lactis
C. albicans
S. pombe
A. niger
1001
1050
AGCGATGAAA TCGCAGACTT AC.TCTACAA CTGGTTCAGT AATTCTATTC
AGTGACGAAG TTGCTGATCT TC.ATTACAA CGGATTTTCC AACTCTATTC
AGTGATACGA TTGCTGATTT AC.ATTATAA TGGGTTTTCA AATAGTATTT
GATGATGAGA CTGCCGACCG CC.ATTACAA CGGATTTAGT AACAGCATTC
CTGAAGGCGC TTGCTTGCTG ACGGATATCC ACTGCTCACA GACTCCATTC
1051
1100
1101
1150
conserved regions
1651
1700
1701
1750
FIG. 5
6/13

FIGUR 6

SEQ ID NO:8 (nucleic acid sequence)
SEQ ID NO:7 (amino acid sequence)

```
-792  CTTAAATACCACAATAGGAAAATTATCAATAAAGCTTTTCGGATTTCATTACGTTATATC -733
-732  GCAAAAAAATAGTCGAGCTTTCTGAACCGTTCGTTAATAAAAAAATAGTTTTTTCAGATT -673
-672  TCTATGTGAGGCAGTCACGATAGAATTCCATCGAACTCGTCAGCGCCAAATGTGAATGCG -613
-612  GCTTTCAAAAGCTTTGTCGAATTTGGGATGGGAATCCATGAATCGAAGATGTCAAAATGG -553
-552  GGGATCACAAAAGTACACTCACGAGGAAAATCAAAACCTTCTCGTACCTTTAACACATAC -493
-492  GGAAATGATCGATCGATTTGAGAAGATTCCTCAATGATTTTCGTCATATATAGGTATCTG -433
-432  AGGTATTTATGGACCGATTCGTAATAACATCATATACATCGCGCTTTGTCCCTGTCCCAG -373
-372  AGATTTCGATGAAAAAAGCGAATTTTATTCTAATATTTGAAGCATGCCAAACATGGGGCA -313
-312  GTTGATTTGTGTGAGGGTAAAATATCATGAATTGCACCCATCAAATGCAGCAAGATATTG -253
-252  ACCAATCCTATAATAGAAAACAGACTTACCACAAATAGATTGTGATGACGATATTATGAA -193
-192  TCTCCAGATGAAAGGCTCGAAAGCTATGAAGCCTCTTGAAACTTTTCATGGTGAGATAAT -133
-132  ATTTTCGAAATTTCCACGAACTTCTAAAACGCAATTATTGAATATAAAGGAAAAATAATA -73
 -72  TTTCCATATAGCAAGCAAATCAAGCTGCACTCCTCATCCTTAAAACTAATAAATCTTACC -13
 -12  CATTTGATACCAATGGTCAAAGGTAATGTTATAGTGGTTTCAAATAGAATCCCAGTCACT  48
   1                 MetValLysGlyAsnValIleValValSerAsnArgIleProValThr  16

  49  ATTAAGAAGACTGAAGATGATGAAAATGGAAAATCAAGATACGACTATACAATGTCATCA 108
  17  IleLysLysThrGluAspAspGluAsnGlyLysSerArgTyrAspTyrThrMetSerSer  36

 109  GGCGGATTAGTGACGGCATTACAAGGGCTCAAAAATCCATTTCGATGGTTTGGATGGCCT 168
  37  GlyGlyLeuValThrAlaLeuGlnGlyLeuLysAsnProPheArgTrpPheGlyTrpPro  56

 169  GGGATGTCTGTTGATAGCGAACAGGGACGACAAACTGTCGAGCGGGATTTGAAGGAAAAG 228
  57  GlyMetSerValAspSerGluGlnGlyArgGlnThrValGluArgAspLeuLysGluLys  76

 229  TTCAATTGTTATCCGATATGGTTAAGTGACGAAATTGCAGACTTACATTATAACGGCTTT 288
  77  PheAsnCysTyrProIleTrpLeuSerAspGluIleAlaAspLeuHisTyrAsnGlyPhe  96

 289  AGCAATTCTATACTTTGGCCATTGTTCCACTATCACCCAGGGGAGATGAATTTTGATGAA 348
  97  SerAsnSerIleLeuTrpProLeuPheHisTyrHisProGlyGluMetAsnPheAspGlu 116

 349  ATTGCTTGGGCCGCTTATTTGGAAGCAAATAAACTGTTTTGCCAAACGATCTTAAAGGAG 408
 117  IleAlaTrpAlaAlaTyrLeuGluAlaAsnLysLeuPheCysGlnThrIleLeuLysGlu 136

 409  ATAAAAGACGGGGACGTTATCTGGGTACATGATTATCATCTCATGTTGTTGCCTTCACTG 468
 137  IleLysAspGlyAspValIleTrpValHisAspTyrHisLeuMetLeuLeuProSerLeu 156

 469  CTAAGAGACCAACTTAATAGTAAGGGGCTACCGAATGTCAAAATTGGCTTTTTCCTTCAT 528
 157  LeuArgAspGlnLeuAsnSerLysGlyLeuProAsnValLysIleGlyPhePheLeuHis 176

 529  ACTCCTTTTCCTTCAAGCGAAATATACAGGATACTTCCTGTAAGGAAAGAAATTCTCGAA 588
 177  ThrProPheProSerSerGluIleTyrArgIleLeuProValArgLysGluIleLeuGlu 196

 589  GGAGTGCTTAGTTGTGATTTGATAGGTTTCCACACCTATGATTATGTCCGTCACTTTCTT 648
 197  GlyValLeuSerCysAspLeuIleGlyPheHisThrTyrAspTyrValArgHisPheLeu 216

 649  AGTTCGGTTGAAAGAATATTGAAATTGCGAACGAGCCCACAAGGTGTTGTCTATAATGAT 708
 217  SerSerValGluArgIleLeuLysLeuArgThrSerProGlnGlyValValTyrAsnAsp 236
```

FIGUR 6
(cont.)

```
709  AGACAGGTGACTGTAAGTGCTTATCCGATTGGCATTGACGTTGACAAATTCTTGAATGGT  768
237  ArgGlnValThrValSerAlaTyrProIleGlyIleAspValAspLysPheLeuAsnGly  256

769  CTTAAGACTGATGAGGTCAAAAGCAGGATAAAACAGCTGGAAACCAGATTTGGTAAAGAT  828
257  LeuLysThrAspGluValLysSerArgIleLysGlnLeuGluThrArgPheGlyLysAsp  276

829  TGTAAACTTATTATTGGGGTGGACAGGCTGGATTACATCAAAGGTGTACCTCAAAAACTC  888
277  CysLysLeuIleIleGlyValAspArgLeuAspTyrIleLysGlyValProGlnLysLeu  296

889  CACGCGTTTGAAATTTTCTTGGAGAGACACCCTGAGTGGATTGGAAAAGTTGTTTTGATA  948
297  HisAlaPheGluIlePheLeuGluArgHisProGluTrpIleGlyLysValValLeuIle  316

949  CAGGTGGCTGTCCCCTCACGAGGGGACGTTGAAGAATATCAATCTTTGAGGGCAGCTGTA 1008
317  GlnValAlaValProSerArgGlyAspValGluGluTyrGlnSerLeuArgAlaAlaVal  336

1009 AATGAGCTAGTGGGAAGAATCAATGGTAGATTTGGTACCGTCGAATTTGTTCCTATCCAT 1068
337  AsnGluLeuValGlyArgIleAsnGlyArgPheGlyThrValGluPheValProIleHis  356

1069 TTCCTTCATAAAAGCGTGAACTTCCAAGAGCTGATATCTGTCTACGCTGCTAGTGATGTT 1128
357  PheLeuHisLysSerValAsnPheGlnGluLeuIleSerValTyrAlaAlaSerAspVal  376

1129 TGTGTAGTGTCATCGACACGGGACGGAATGAATTTGGTCAGTTATGAATACATTGCTTGT 1188
377  CysValValSerSerThrArgAspGlyMetAsnLeuValSerTyrGluTyrIleAlaCys  396

1189 CAACAAGATCGAAAGGGATCTCTAGTACTAAGTGAATTTGCGGGAGCTGCTCAGTCATTA 1248
397  GlnGlnAspArgLysGlySerLeuValLeuSerGluPheAlaGlyAlaAlaGlnSerLeu  416

1249 AATGGCGCTCTCGTAGTGAATCCATGGAATACAGAAGAACTCAGTGAAGCTATTTACGAA 1308
417  AsnGlyAlaLeuValValAsnProTrpAsnThrGluGluLeuSerGluAlaIleTyrGlu  436

1309 GGCTTGATCATGAGTGAAGAGAAAAGGAGGGGCAATTTTCAGAAGATGTTCAAGTACATT 1368
437  GlyLeuIleMetSerGluGluLysArgArgGlyAsnPheGlnLysMetPheLysTyrIle  456

1369 GAGAAATATACTGCAAGTTATTGGGGAGAGAACTTTGTGAAAGAATTGACGAGAGTGTGA 1428
457  GluLysTyrThrAlaSerTyrTrpGlyGluAsnPheValLysGluLeuThrArgVal      476

1429 TTACTGTGGTTTGCAGGTTAATTTGAAATGTTCACTTGTACTTGAAGAATTTTATATTAT 1488
1489 ATACATGTTATACATCAATAGGATAAAAATTAAGTAGACAAAGTTATCATTTTGTTGGGC 1548
1549 TGTAAAAATTGAACGATAACAATATATTTGACAAAATTAATTTGATCTAATTGAGCTGGA 1608
1609 GGGCGTAATATATTTGGTTTCCTGAATCATCTTGTAGATCACAATATGGGGCAGCTTCTT 1668
1669 TCGCAGCCGATCACAGAGAAACACATCACACTTGTCCAACATGATCACATATCGCATTCA 1728
1729 ATCGGGGAAATGCAAGGATACAGGTTGACCATGGAAGACGCGTTCTGTGATTTGAACGAA 1788
1789 AGAATATTCGTGACGGAAGAGGGACTTGACATCAGAAAACAAGACGAGAATACAGAGGGT 1848
1849 GATCTGGAGTCTCTTCAAATTAACATTTATGGTGTCTTTGACGGACATGGCGGTT       1903
```

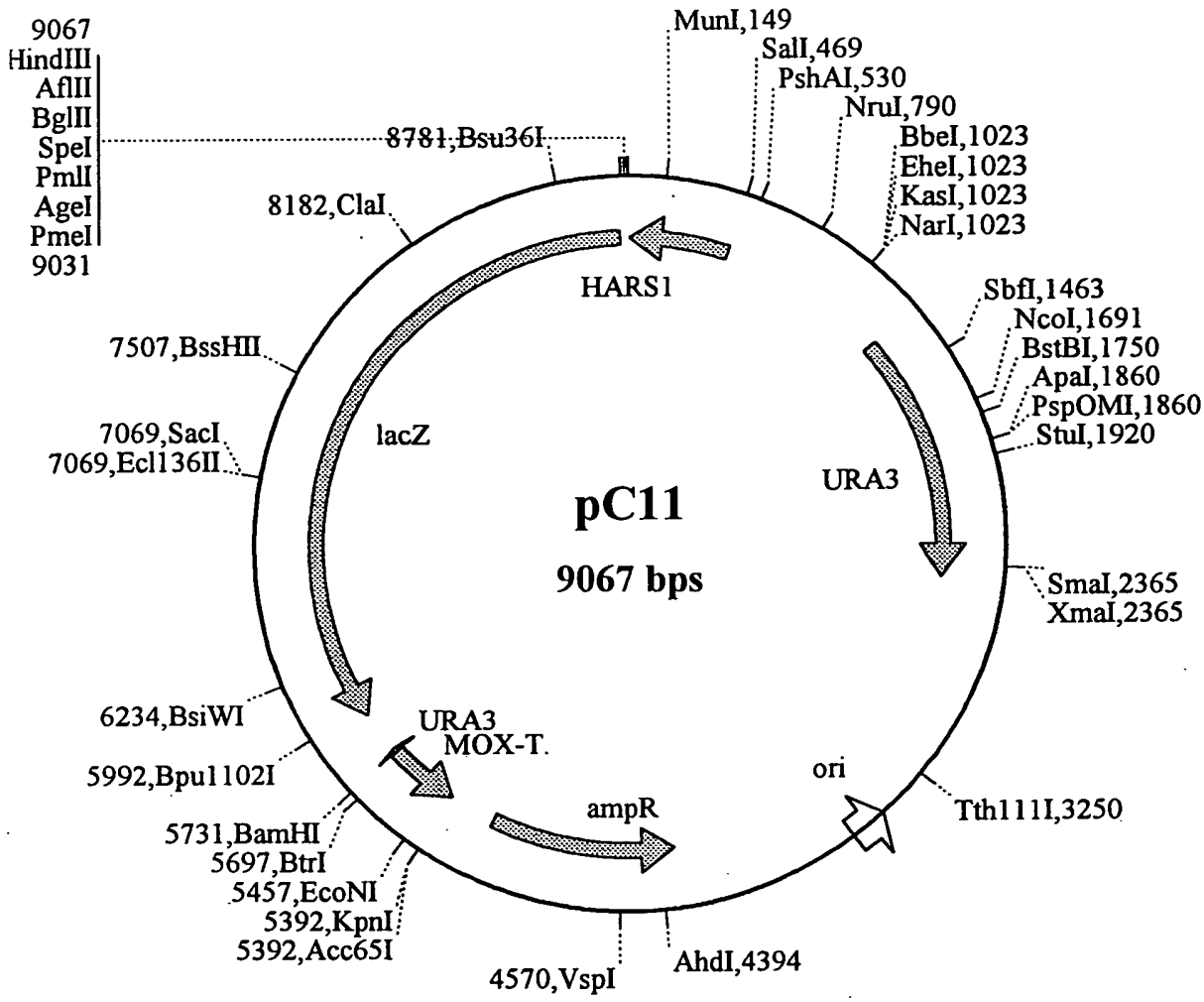

9067
HindIII
AflII
BglII
SpeI
PmlI
AgeI
PmeI
9031
8781,Bsu36I
MunI,149
SalI,469
PshAI,530
NruI,790
BbeI,1023
EheI,1023
KasI,1023
NarI,1023
8182,ClaI
HARS1
SbfI,1463
NcoI,1691
BstBI,1750
ApaI,1860
PspOMI,1860
StuI,1920
7507,BssHII
7069,SacI
7069,Ecl136II
lacZ
URA3
pC11
9067 bps
SmaI,2365
XmaI,2365
6234,BsiWI
URA3
MOX-T.
5992,Bpu1102I
ampR
ori
Tth111I,3250
5731,BamHI
5697,BtrI
5457,EcoNI
5392,KpnI
5392,Acc65I
4570,VspI
AhdI,4394

FIG. 7

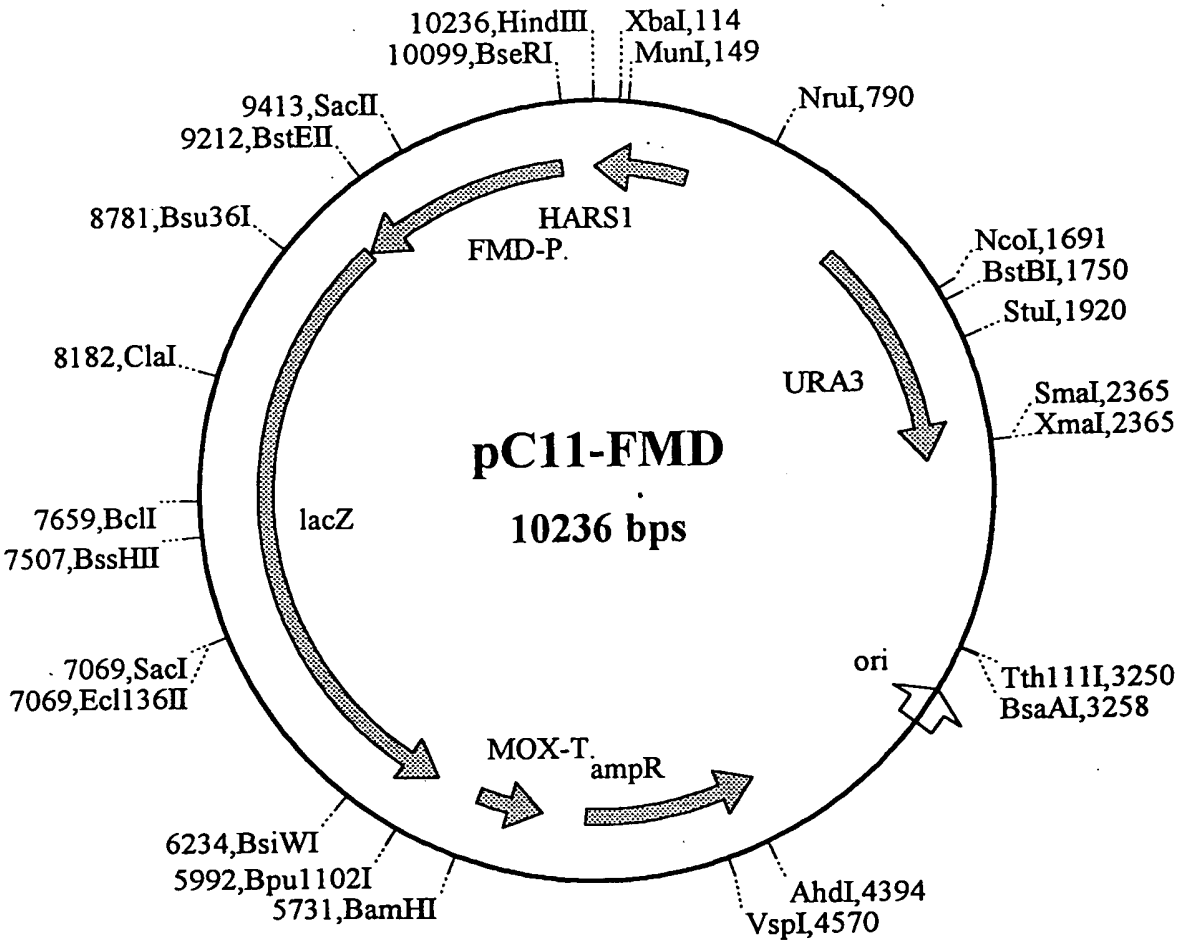

10236,HindIII
XbaI,114
10099,BseRI
MunI,149
NruI,790
9413,SacII
9212,BstEII
8781,Bsu36I
HARS1
FMD-P.
NcoI,1691
BstBI,1750
StuI,1920
8182,ClaI
URA3
SmaI,2365
XmaI,2365
pC11-FMD
10236 bps
7659,BclI
7507,BssHII
lacZ
7069,SacI
7069,Ecl136II
ori
Tth111I,3250
BsaAI,3258
MOX-T.
ampR
6234,BsiWI
5992,Bpu1102I
5731,BamHI
AhdI,4394
VspI,4570

FIG. 8

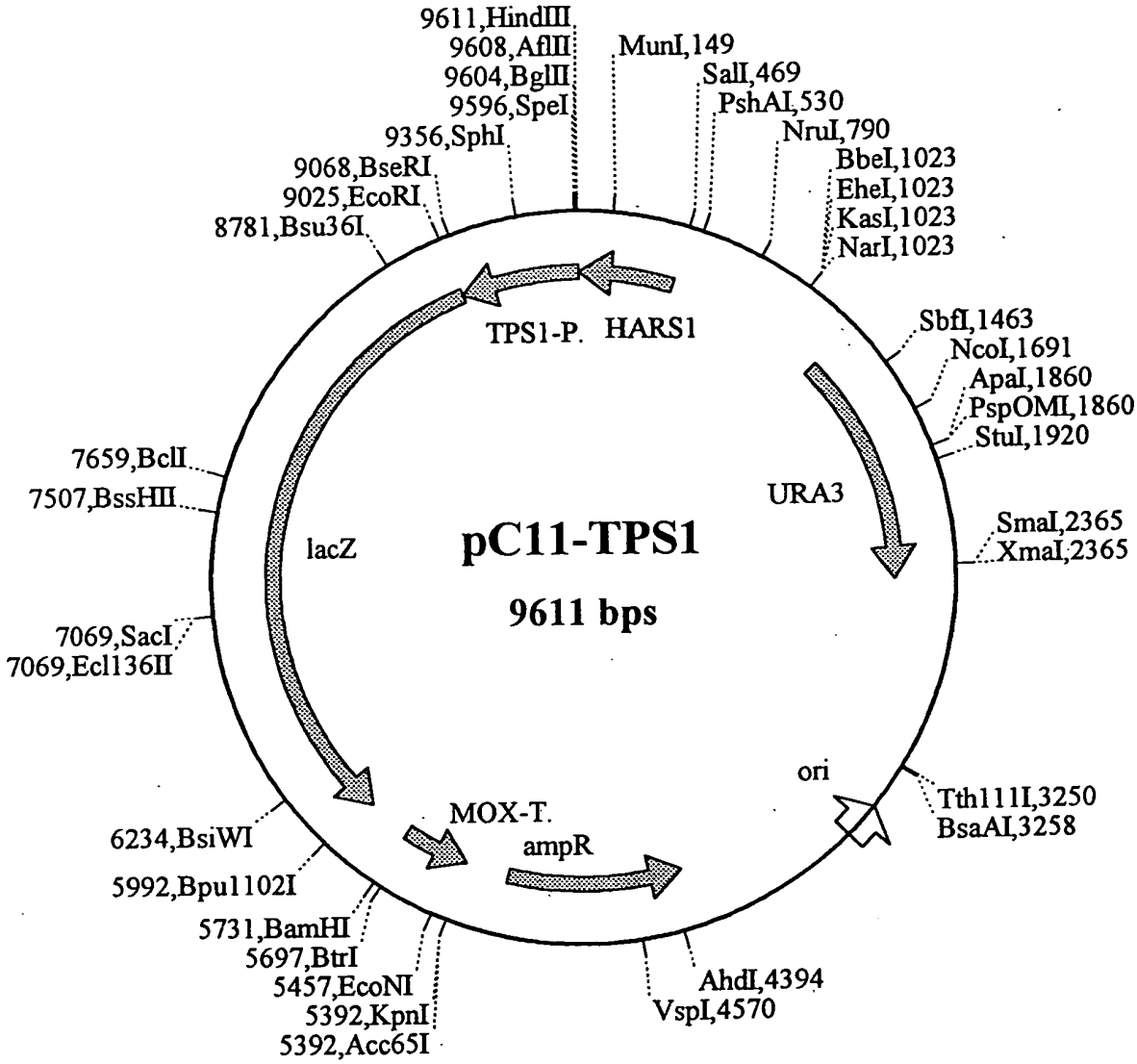

9611,HindIII
9608,AflII
9604,BglII
9596,SpeI
MunI,149
SalI,469
PshAI,530
NruI,790
BbeI,1023
EheI,1023
KasI,1023
NarI,1023
9356,SphI
9068,BseRI
9025,EcoRI
8781,Bsu36I
TPS1-P.
HARS1
SbfI,1463
NcoI,1691
ApaI,1860
PspOMI,1860
StuI,1920
7659,BclI
7507,BssHII
URA3
lacZ
pC11-TPS1
9611 bps
SmaI,2365
XmaI,2365
7069,SacI
7069,Ecl136II
ori
Tth111I,3250
BsaAI,3258
MOX-T.
ampR
6234,BsiWI
5992,Bpu1102I
5731,BamHI
5697,BtrI
5457,EcoNI
5392,KpnI
5392,Acc65I
AhdI,4394
VspI,4570

FIG. 9

FIG. 10A

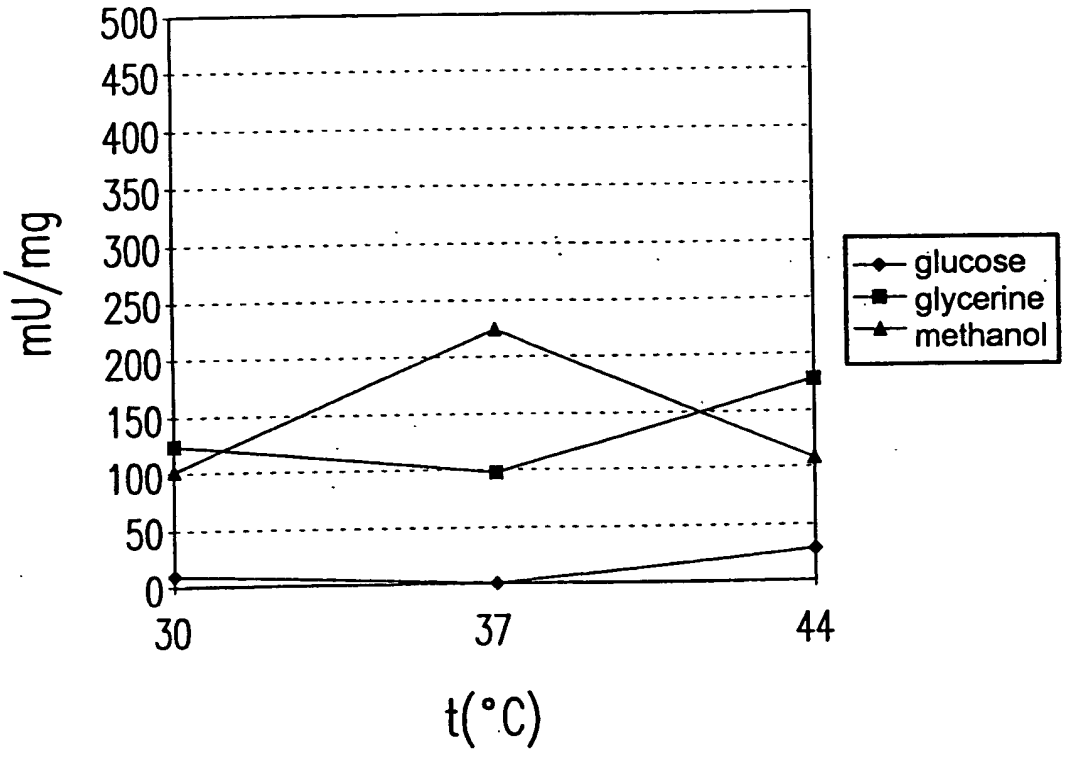
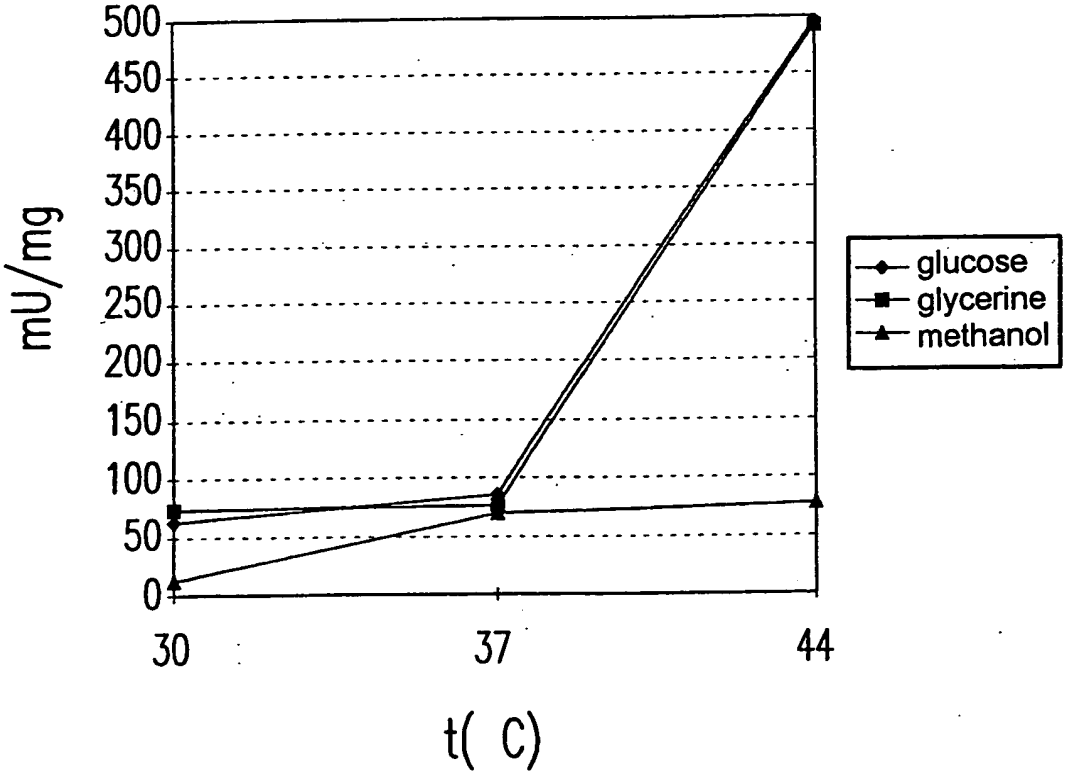


FIG. 10B



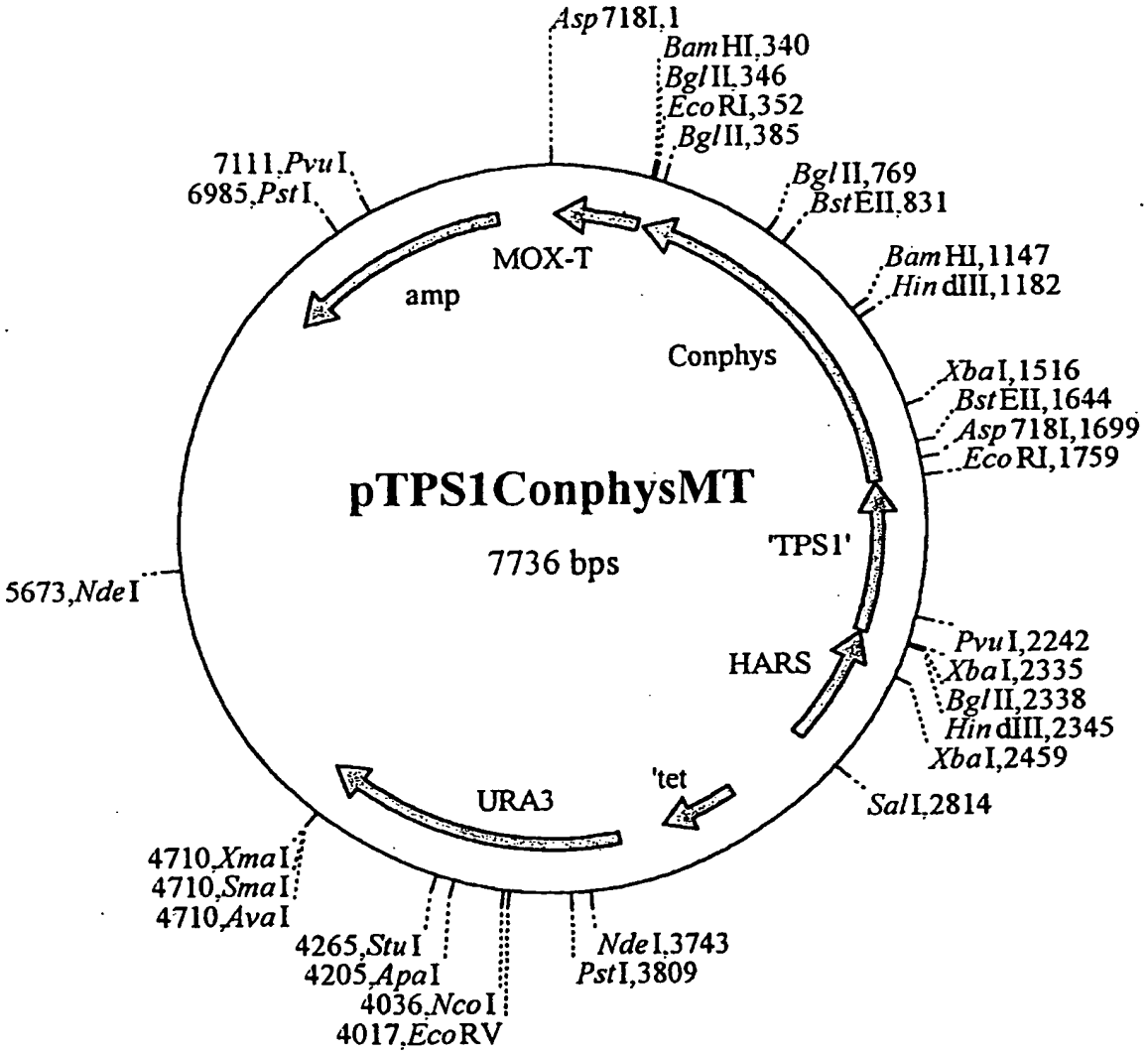

Asp718I,1
BamHI,340
BglII,346
EcoRI,352
BglII,385
BglII,769
BstEII,831
BamHI,1147
HindIII,1182
XbaI,1516
BstEII,1644
Asp718I,1699
EcoRI,1759
PvuI,2242
XbaI,2335
BglII,2338
HindIII,2345
XbaI,2459
SalI,2814
NdeI,3743
PstI,3809
4265,StuI
4205,ApaI
4036,NcoI
4017,EcoRV
4710,XmaI
4710,SmaI
4710,AvaI
5673,NdeI
7111,PvuI
6985,PstI
MOX-T
amp
Conphys
pTPS1ConphysMT
7736 bps
'TPS1'
HARS
'tet
URA3

FIG. 11